

## Research Article

# Yield and Mineral Composition among Mungbean [*Vigna radiata* (L.) R. Wilczek] Genotypes Grown in Different Agroecologies in East Africa

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Mungbean [*Vigna radiata* (L.) R. Wilczek var. *radiata*] also referred to as green gram is a key crop especially in the marginal areas of East Africa. It is rich in micronutrients and protein and thus can help ameliorate malnutrition if incorporated into diets. This study was conducted to evaluate the performance of 26 fixed elite mungbean breeding genotypes for yield and micronutrient composition across different locations in East Africa (Uganda, Kenya, and Tanzania). The genotypes displayed significant variability for nutritional, phenology, and yield-related traits across test environments. Significant genotype effects were observed for most of the traits except for average yield per plant and dry matter content ( $P < 0.05$ ). Random effect of environment was significant for all traits, and significant GXE was observed for all traits except for dry matter and iron content ( $P < 0.05$ ). Moderate to high broad-sense heritability ( $H^2$ ) was found among traits except for dry matter content which was low ( $H^2 = 10.4\%$ ). There was a significant and positive correlation between Fe and Zn ( $r = 0.58$ ), and Fe and Ca ( $r = 0.46$ ), indicating the potential to enhance these traits simultaneously through breeding and/or selection. However, the correlation between yield and nutrients (iron, zinc, and calcium) was negative. Environments KAT\_SR\_2019, KYM\_LR\_2020, and KYM\_LR\_2020 were found to be discriminating (informative) and representative of grain yield, calcium, and zinc content, respectively. Genotypes AVMU 1679, AVMU 1685, and AVMU 1686 combined both stability and high micronutrient content, while the high yielding and stable genotypes were AVMU 1689, AVMU 1681, and AVMU 16102. The identified genotypes need to be assessed for farmer preference in on-farm trials before they can be recommended for release as new varieties. Additionally, these genotypes will be useful in future breeding efforts as donors aimed at developing nutrient-dense and high yielding mungbean varieties.

## 1. Introduction

Mungbean [*Vigna radiata* (L.) R. Wilczek var. *radiata*], also known as green gram, is a key food and cash crop in several parts of the world especially in Asia and East Africa. Its short maturity period, low input requirements, drought tolerance, and ability to improve soil fertility through nitrogen fixation

makes it an ideal crop for low input production systems [1]. Nutritionally, mungbean grain is a rich source of essential nutrients such as protein (up to 31%), iron ( $>8.7$  mg/100 g), and zinc (up to 6.2 mg/100 g) [2, 3]. In addition to being an excellent protein and mineral source, mungbean contains less flatulence causing factors compared to other legumes. This makes it an ideal food for children and the convalescing

[4]. Mungbean starch is also highly digestible with a high glycemic index and thus more suitable for malnourished patients [5].

Malnutrition is a serious global health concern, especially in developing countries. For instance, in 2020, it is projected that between 720 and 811 million people in the world were hungry. During the same period, more than half of the world's undernourished were found in Asia (418 million) and more than one-third in Africa (282 million) [6]. Micronutrient malnutrition is a major concern affecting especially women and children [7]. Iron deficiency is the most prevalent form of nutritional disorder affecting mainly the poorest and vulnerable populations in resource-constrained environments in developing countries [8]. For instance, in 2019, the incidence of iron deficiency anaemia in East Africa was 53%, 31%, and 39% among children (<5 years), nonpregnant women, and pregnant women, respectively [8]. Zinc deficiency is an equally widespread public health concern in low and middle income countries (LMICs). Zinc deficiency tends to coexist with iron deficiency because of an overlap of food sources and dietary factors inhibiting the intake of the two nutrients [9].

Mitigating iron and zinc deficiencies through food fortification and food supplements has been less successful in curbing the scourge of mineral deficiencies due to poor health infrastructure and low purchasing power [10]. A food-based approach that promotes the cultivation and consumption of popular nutrient-rich crops/foods is a more cost-effective and sustainable approach [10]. Mungbean is a popular short duration and drought-tolerant legume crop cultivated by smallholder farmers across East Africa both for food and farm income generation. This study was, therefore, initiated to determine the genetic variation of iron, zinc content, and yield among 26 fixed elite mungbean genotypes grown in contrasting environments in Uganda, Kenya, and Tanzania.

## 2. Materials and Methods

**2.1. Planting Materials.** Twenty-six (26) fixed elite mungbean genotypes introduced from the World Vegetable Center, formerly known as the Asian Vegetable Research and Development Center (AVRDC), were evaluated in this study (Table 1). The elite genotypes were selected from NM 94 × CN 9-5, CN 9-5 × NM 94, and Harsha × NM94 crosses. The parents CN 9-5 and Harsha showed high concentrations of iron (8.7 mg/100 g and 8.1 mg/100 g, respectively) in a previous study [3].

**2.2. Trial Locations and Experimental Design.** Field trials were established at three sites in Kenya (Ithookwe, Kampiyamawe, and Katumani) during the short rainy season of 2019 (SR2019), the long rainy season of 2020 (LR2020), and three sites in Uganda (Serere, Lira, and Arua) during the second season of 2019 (2019B) and first season of 2020 (2020A). In Tanzania, trials were established at four sites (Miwaleni, Ilonga, Ukiriguru, and Tenguru) during 2019B season (Table 2). Each location and season combination

TABLE 1: List of AVRDC elite mungbean genotypes evaluated in the study.

Entry no.	Entry name	Seed colour	Luster
1	AVMU 16100	Green	Shiny
2	AVMU 16101	Green	Shiny
3	AVMU 16102	Green	Shiny
4	AVMU 16103	Green	Shiny
5	AVMU 16104	Green	Shiny
6	AVMU 16105	Green	Shiny
7	AVMU 1677	Green	Shiny
8	AVMU 1678	Green	Shiny
9	AVMU 1679	Green	Shiny
10	AVMU 1680	Green	Shiny
11	AVMU 1681	Green	Shiny
12	AVMU 1682	Green	Shiny
13	AVMU 1683	Green	Shiny
14	AVMU 1684	Green	Shiny
15	AVMU 1685	Green	Shiny
16	AVMU 1686	Green	Shiny
17	AVMU 1687	Green	Shiny
18	AVMU 1688	Green	Shiny
19	AVMU 1689	Green	Shiny
20	AVMU 1690	Green	Shiny
21	AVMU 1694	Green	Shiny
22	AVMU 1695	Green	Shiny
23	AVMU 1696	Green	Shiny
24	AVMU 1697	Green	Shiny
25	AVMU 1698	Green	Shiny
26	AVMU 1699	Green	Shiny

constituted a different environment, giving a total of 15 environments in which elite mungbean genotypes were evaluated. The weather conditions of each environment during the cropping cycles are presented in Figures 1(a)–1(c). Field trials were laid out in an alpha design with two replications at each site for each season. In Kenya, one row plots of length two (2) meters with a spacing of 0.6 m × 0.1 m were used for each genotype. In Tanzania, each mungbean genotype was planted in 4 rows of length 3 m at a spacing of 0.5 m × 0.2 m. In Uganda, the genotypes were planted in 2 rows each 2 meters long with a spacing of 0.5 m × 0.2 m. At each trial site, planting, weeding, thinning, pest management, and harvesting were carried out manually. Pods harvested from each plot were sun-dried before manual threshing. Threshed grain was dried to a moisture content of 13% before determining the plot grain weight.

### 2.3. Data Collection

**2.3.1. Preplanting Soil Characterization.** Before planting at each trial location, soil samples were collected at a depth of 0–20 cm for laboratory analysis. Soil samples were first air-dried, then pounded, and later sieved through a 2 mm sieve to remove any debris and then subjected to physical and chemical analyses following standard methods described by Okalebo et al. [11]. Soil pH was measured in a soil-to-water solution ratio of 1 : 2.5; organic matter (organic carbon) by potassium dichromate wet acid oxidation method; total N was determined by Kjeldhal digestion; extractable P by Bray

TABLE 2: Characteristics of trial sites used in the evaluation of mungbean genotypes.

Country	Location	Environment	Latitude	Longitude	Altitude (m)
Kenya	Ithookwe	ITHOOKWE_SR_2019	1° 22'S	37° 49'E	1122
Kenya	Ithookwe	ITHOOKWE_LR_2020	1° 22'S	37° 49'E	1122
Kenya	Kampiyamawe	KYM_SR_2019	1° 48'S	37°40'E	975
Kenya	Kampiyamawe	KYM_LR_2020	1° 48'S	37°40'E	975
Kenya	Katumani	KAT_SR_2019	1° 35'S	37°14'E	1600
Kenya	Katumani	KAT_LR_2020	1° 35'S	37°14'E	1600
Uganda	Serere	SERERE_2019B	1.536744N	33.447120E	1140
Uganda	Serere	SERERE_2020A	1.536744N	33.447120E	1140
Uganda	Lira	LIRA_2020A	2.297487N	32.914027E	1084
Uganda	Arua	ARUA_2019B	3.078586N	30.947898E	1198
Uganda	Arua	ARUA_2020A	3.078586N	30.947898E	1198
Tanzania	Miwaleni	Miwaleni_2019B	3°26'5''S	37°26'58''E	1102
Tanzania	Ilonga	TARI Ilonga_2019B	-3.25325S	37.26977	737
Tanzania	Ukiriguru	TARI Ukiriguru_2019B	-2.066123S	33.236096E	1265
Tanzania	Tengeru	WVC Tengeru_2019B	-3.37568344S	36.80567603E	1231

P1 method; exchangeable base from an ammonium acetate extract by flame photometry ( $K^+$ ,  $Na^+$ ) and atomic absorption spectrophotometer ( $Ca^{2+}$ ,  $Mg^{2+}$ ,  $Fe$ , and  $Zn$ ); and particle size distribution (texture) using the Bouyoucos (hydrometer) method (Table 3).

**2.3.2. Traits Assessed.** During the field trials, data were collected on the number of days to flowering, number of days to maturity, plant height, pod number, pod length, pod and seed yield, number of seeds per plant, plot seed weight, yield per ha, and seed size (100 seed weight). Plot seed weight was used to compute yield per ha. A description of the trait measurements during field experiments is provided in Table 4.

**2.3.3. Nutrient Analysis of Seed Samples.** From each genotype, 20 g of seeds from a well-mixed dried clean seed pool was sampled after removing damaged seeds and debris. The seed samples were crushed into flakes using a hand hammer or grinder. With the hammer method, the seeds were placed in a paper envelope wrapped completely with a tape. The hammer was then used to crush the samples until the whole seeds were ruptured. The mungbean flakes were then shipped to the laboratory at the World Vegetable Center, Taiwan, for nutrient analysis. Before nutrient analysis, the flakes were processed into a fine powder of uniform size. The samples were analysed for dry matter content, iron, zinc, and calcium. The dry matter of each grain sample was determined from the weight difference of 1.0 g of fine powder before and after placing it in an oven (Model #DN 63, Yamato, Tokyo, Japan) at 135°C for 2 h as described by the authors of [13]. For mineral analysis, ground samples were prepared by wet acid digestion and then analysed using inductively coupled plasma-optical emission spectrometry (ICP-OES) [3].

**2.4. Statistical Analysis.** A combined analysis of variance (ANOVA) was performed across 15 environments (the combination of season and location was treated as an

environment), to assess the main and interaction effects of genotypes and environments, considering genotypes as fixed, and environments as well as replication as random effects. The individual variance of environments was estimated and modelled to an error distribution using REML (residual maximum likelihood estimator) procedure using ASReml v4.2 [14]. BLUPs (best linear unbiased predictors) were estimated for all random effects, and BLUEs were estimated for fixed effects from the combined analysis of variance. Spearman's rank correlation coefficient was calculated to study the relationship among test environments (Spearman's rank correlation), and the Pearson correlation coefficient was used to find the correlation among traits. The GGE biplot site regression model [15] was used to visualize the  $G \times E$  interaction patterns and to distinguish (1) the performance and stability of genotype(s) across all environments (genotype evaluation), (2) discriminating (informative) power and non-crossover interaction among environments (under environmental evaluation), and (3) identify which-won-where patterns where specific genotypes can be recommended to a specific environment(s) (specific adaptability).

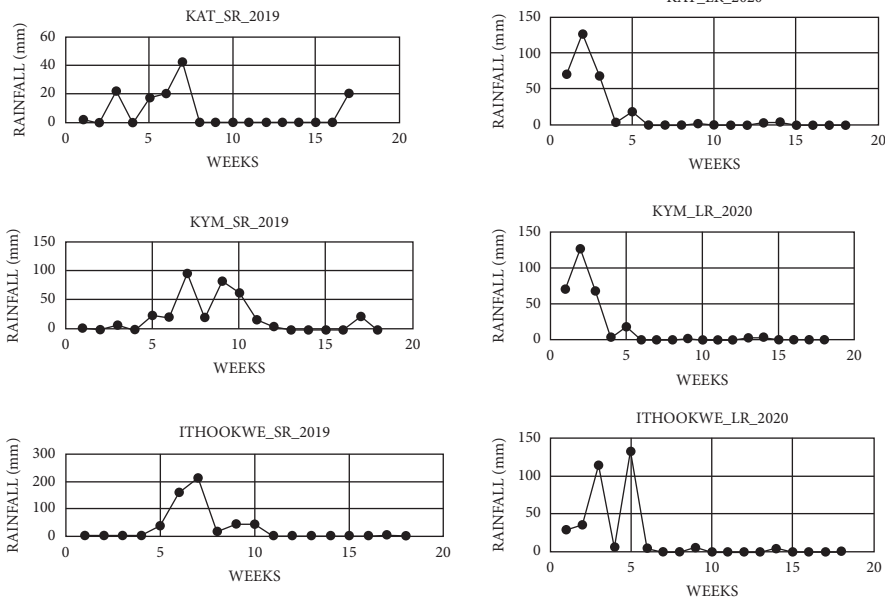
For the estimation of broad-sense heritability ( $H^2$ ) for the pooled data, all factors and genotypes were treated as random terms to estimate the genotypic variance ( $V_G$ ), genotype  $\times$  environment variance ( $V_{G \times E}$ ), and the residual variance ( $V_E$ ) using the following formula:

$$H^2 = \frac{\sigma_g^2}{(\sigma_g^2 + (\sigma_{g \times e}^2 / e) + (\sigma_e^2 / r * e))}, \quad (1)$$

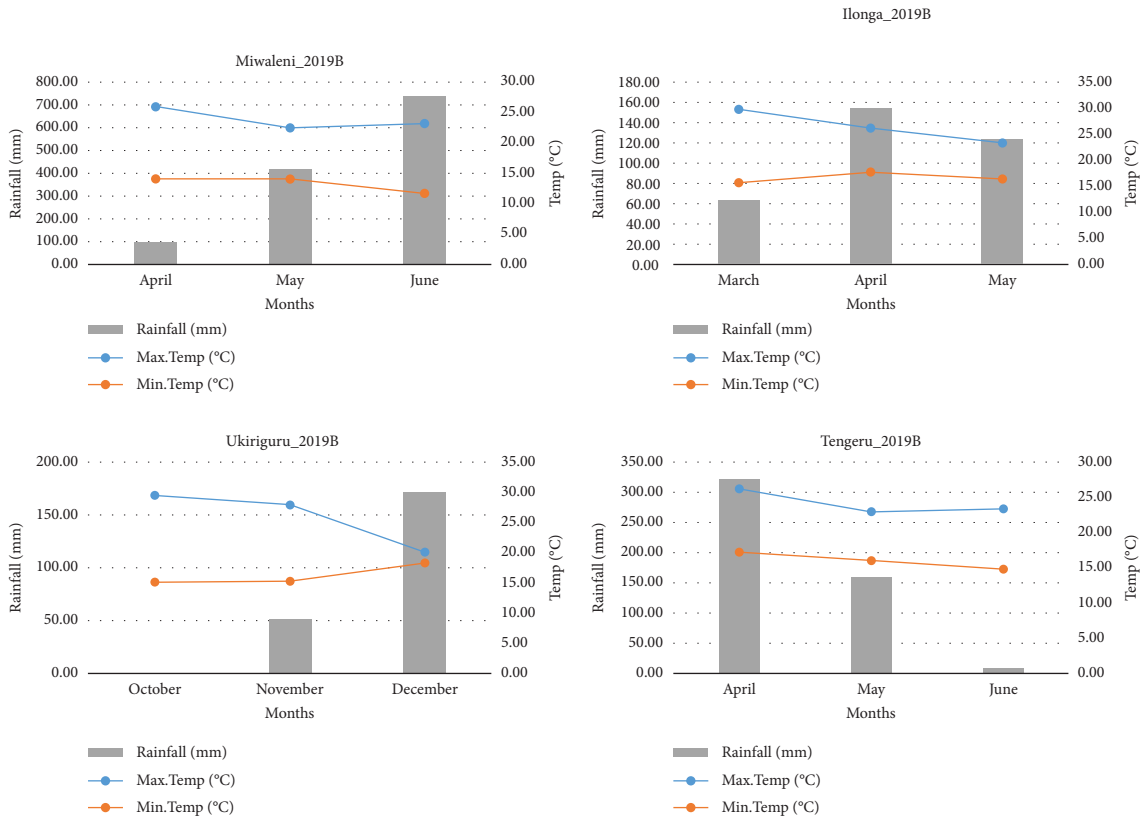
where  $r$  and  $e$  are the number of replications and the number of environments.

### 3. Results

**3.1. Soil Characterization at Trial Sites.** Results of soil nutrient composition at each trial location are presented in Table 3. The soil texture at most experimental sites was sandy clay loam. The pH ranged from 4.73 (at Ithookwe) to 7.52 at Miwaleni in Tanzania. Soil nitrogen was generally low at sites and ranged from 0.08 to 0.3% while organic carbon levels



(a)



(b)

FIGURE 1: Continued.

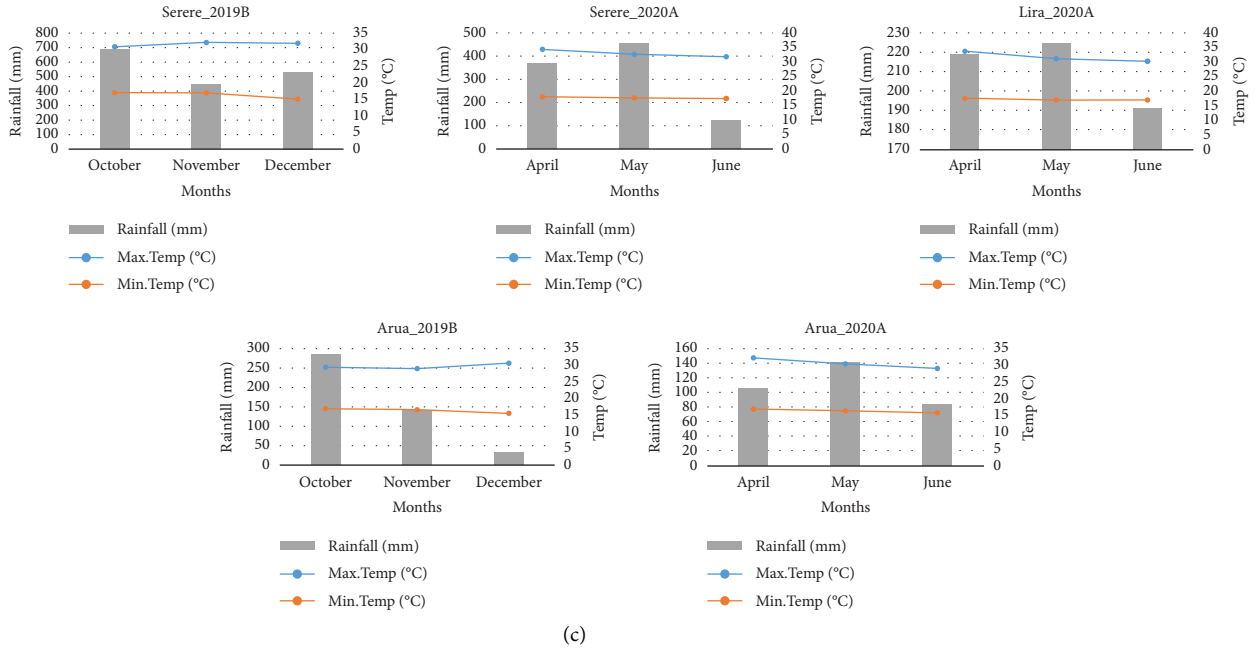


FIGURE 1: (a–c) Rainfall and temperature conditions during cropping cycles in Kenya (a), Tanzania (b), and Uganda (c).

TABLE 3: Soil characteristics at experimental sites in the three countries.

Country	Location	pH	Texture*	%N	%OC	ppm					
						P	K	Ca	Mg	Fe	Zn
Kenya	Ithookwe	4.73	SCL	0.08	0.67	40	132.6	160	24	17.4	1.58
Kenya	Katumani	5.08	SCL	0.10	0.86	70	288.6	520	120	17.7	1.88
Kenya	KampiYaMawe	5.58	SCL	0.12	1.11	60	522.6	560	250.8	19.7	1.82
Uganda	Arua	5.1	SCL	0.3	3.1	T	129	1970	174	195	3.2
Uganda	Lira	6.1	SL	0.1	3.2	T	648	2120	104	127	4.9
Uganda	Serere	5.8	SL	0.3	1.5	T	169	1030	112	132	T
Tanzania	Miwaleni	7.52	Clay	0.084	1.31	71.14	105.3	1960	250.8	228.1	1.56
Tanzania	Ilonga	6.25	SCL	0.112	0.8	7.26	39.0	652	196.8	44.65	1.01
Tanzania	Ukiriguru	7.04	SC	0.112	1.10	5.84	66.3	1838	140.4	24.57	0.64
Tanzania	Tengeru	6.46	Clay	0.189	2.41	40.7	132.6	1218	192	131.87	6.01
Tanzania	Selian	6.91	SCL	0.210	2.14	55.19	390	1458	220.8	27.41	5.48

\*SCL: sandy clay loam; SL: sandy loam; SC: sandy clay; T: trace amounts.

ranged from 0.67 (Ithookwe, Kenya) to 3.2% (Lira, Uganda). Phosphorus levels were low for trial sites in Uganda (Arua, Serere, and Lira) but were largely high for sites in Tanzania and Kenya. Potassium levels were low in the majority of trial sites except in Katumani, Kampi Ya Mawe, Lira (2020A), and Selian where the values were high (>250 ppm). There was also variation in the calcium levels ranging from 160 ppm to 2120 ppm. Iron levels were generally high in Uganda but lowest in Kenya. Similarly, zinc content was high in Ugandan sites compared to Kenya and Tanzania. Generally, testing sites that were moderately acidic had a higher concentration of available nutrients especially iron and zinc.

3.2. Performance of Mungbean Genotypes across Environments. Our findings demonstrated that there was appreciable variation among mungbean genotypes for the

traits studied in the different environments. For instance, TARI\_Ilonga\_2019B and TARI\_Ukiriguru\_2019B had both the lowest and highest number of days to 50% flowering (DFF) and days to maturity (DM), respectively (Figure 2 and Table 5). DFF ranged from 32 days in TARI\_Ilonga\_2019B to 65 days in TARI\_Ukiriguru\_2019B. Genotype AVMU 1686 took the shortest time to reach maturity in Ilonga while AVMU 16103 took the most number of days to reach 50% flowering in Ukiriguru. DM ranged from 60 days in Ilonga to 95 days in Ukiriguru. In the case of plant height (PH), the shortest plant height was recorded in Serere\_2020A while the highest plants were observed in Ithookwe\_SR\_2019. Number of pods per plant (NP) was lowest in ARUA\_2019B (8 pods) and highest in KYM\_SR\_2019 (52 pods per plant). The shortest pods were recorded on genotypes planted in ARUA\_2020A (6.3 cm) while Miwaleni\_2019B registered the highest pod length

TABLE 4: Description of traits measured in field evaluation of mungbean genotypes.

Trait	Code	Description	Stage of observation
Days to 50% flowering	DFP	Number of days from planting to when at least 50% of the plants in a plot have at least one unopened flower	Flowering
Plant height (cm)	PH	Recorded on 5 randomly sampled plants per plot	Physiological maturity
Days to maturity	DM	Days from sowing to when 90% of pods in a plot change colour (to black or brown)	Physiological maturity
Pods per plant	NP	Mean number of pods from 5 random plants per plot	After harvest
Pod length (cm)	PL	Mean lengths measured from five randomly selected pods from each plant (up to 5 plants)	After harvest
Pod yield per plant (g)	PY	Mean weight for all pods measured from five randomly selected plants	After harvest
Number of seeds per pod	NS	Mean number of seeds counted from five randomly selected pods from each plant (up to 5 plants)	After harvest
Seed yield per plant (g)	SY	Mean weight for all seeds measured from five randomly selected plants	After threshing
Plot seed weight (g)	PSW	Weight of all seeds from all plants in a plot	After threshing
Yield (kg)	SYHa	Weight of seeds per ha	After threshing
100 seed weight (g)	100SW	Weight of 100 randomly selected seeds	After threshing

Source: IBGPR [12].



FIGURE 2: Variation in days to maturity (DM), yield (SYHa), iron (Fe), and zinc (Zn) across environments.

(8.8 cm). ARUA\_2020A also had the lowest number of seeds per pod (NS) with about 6.6 seeds per pod, while Ithookwe\_LR\_2020 gave the highest number (10 seeds per pod). Pod yield per plant (PY) was lowest in SERERE\_2020A followed by ARUA\_2020A and ARUA\_2019B, while KYM\_SR\_2019 had the highest pod yield. Seed yield per plant (SY) was equally lowest in ARUA\_2020A and SERERE\_2020A. ARUA\_2020A registered the smallest seed size or 100 seed weight (SW\_100) among all the test environments with 3.83 g/100 seeds, while Lira\_2020A registered

the largest seed size of 5.3 g/100 seeds. Grain yield per hectare was lowest in ARUA\_2020A and highest in ITHOOKWE\_LR\_2020 with values of 613 kg/ha and 2363 kg/ha, respectively. In terms of dry matter composition, small differences were observed among environments. Calcium, iron, and zinc content levels were lowest in ITHOOKWE\_LR\_2020 at 105 mg/100 g, 6.1 mg/100 g, and 2 mg/100 g, respectively while the environment with the highest calcium and iron levels was TARI Ukiriguru\_2019B (Figure 2, S1–S3, and Table 5). Generally, sites/

TABLE 5: Environment mean values (BLUPs) across genotypes for agronomic and mineral traits (per 100 g edible portion of seed on dry weight basis).

#	ENV	DFE	DM	PH	NP	PL	NS	PY (g)	SY (g)	SW_100 (g)	SYHa (kg/ha)	Dry matter (g/100g)	Ca (mg/100g)	Fe (mg/100g)	Zn (mg/100g)
1	ARUA_2019B	45.4	73.5	—	7.669	6.7	7.3	6.3	4.8	4.3	1,267.4	—	—	—	—
2	ARUA_2020A	40.9	79.0	26.9	10.9	6.3	6.6	6.2	3.1	3.8	612.8	—	—	—	—
3	ITHOOKWE_LR_2020	39.7	71.9	49.7	37.0	8.4	10.3	23.7	14.2	4.9	2,363.2	86.7	105.0	6.1	2.0
4	ITHOOKWE_SR_2019	41.5	73.8	49.7	39.4	7.9	9.9	24.2	12.8	4.6	1,840.6	87.5	126.1	6.6	2.4
5	KAT_LR_2020	46.9	87.2	29.9	24.4	7.6	8.9	12.6	8.4	4.9	1,113.1	87.3	114.4	6.5	2.6
6	KAT_SR_2019	45.7	85.2	42.9	32.6	7.8	9.2	14.7	8.5	4.6	1,421.8	87.6	128.4	7.0	2.8
7	KYM_LR_2020	40.1	72.2	36.6	26.8	7.7	8.0	17.4	10.6	4.7	1,803.7	87.2	109.1	7.1	2.5
8	KYM_SR_2019	43.8	77.2	49.6	51.8	7.7	9.4	27.5	10.6	4.7	1,803.4	87.7	117.8	6.5	2.4
9	LIRA_2020A	38.0	69.1	25.9	21.0	7.0	8.4	12.7	6.4	5.3	1,281.7	86.5	109.1	8.2	3.4
10	Miwaleni_2019B	40.0	75.1	33.8	14.9	8.8	—	—	5.3	5.0	1,028.9	—	—	—	—
11	SERERE_2019B	36.9	62.9	—	9.7	7.3	8.1	8.1	6.0	4.1	1,206.2	—	—	—	—
12	SERERE_2020A	35.3	62.7	22.6	9.3	6.9	7.3	4.8	3.2	4.6	631.5	86.9	131.3	7.3	3.4
13	TARI Ilonga_2019B	32.0	60.2	31.1	15.4	7.6	—	—	4.8	4.8	960.2	—	—	—	—
14	TARI Ukiriguru_2019B	64.7	94.9	32.8	20.4	8.2	—	—	6.0	4.8	1,198.1	87.8	160.4	8.8	3.2
15	WVC Tengeru_2019B	44.6	90.6	26.3	14.6	7.7	—	—	5.4	4.3	749.5	87.4	132.8	8.5	2.9
	$F^2$	45.4	67.8	40.9	55.6	83.4	61.7	44.6	25.9	83.6	38.3	10.4	74.4	49.4	47.9
	CV	5.5	2.3	10.4	20.5	9.1	10.9	10.7	32.3	11.8	14.9	0.5	10.1	19.4	9.6



TABLE 6: Genotype mean values (BLUEs) across the environments for different traits evaluated in the study (mean  $\pm$  SE).

Genotype	Gen#	DFF	DM	PH	NP	PL	NS	PY
AVMU 16100	1	43.4 $\pm$ 2.0	76.5 $\pm$ 2.7	32.0 $\pm$ 3.1	21.9 $\pm$ 4.1	7.5 $\pm$ 0.2	8.7 $\pm$ 0.5	13.5 $\pm$ 3.1
AVMU 16101	2	43.3 $\pm$ 2.0	76.9 $\pm$ 2.7	32.4 $\pm$ 3.1	22.0 $\pm$ 4.1	6.8 $\pm$ 0.2	9.3 $\pm$ 0.5	12.9 $\pm$ 3.0
AVMU 16102	3	42.1 $\pm$ 2.0	75.5 $\pm$ 2.7	33.9 $\pm$ 3.1	22.3 $\pm$ 4.1	7.7 $\pm$ 0.2	9.0 $\pm$ 0.5	14.2 $\pm$ 3.0
AVMU 16103	4	42.4 $\pm$ 2.0	75.7 $\pm$ 2.7	35.5 $\pm$ 3.1	22.2 $\pm$ 4.1	7.7 $\pm$ 0.2	7.9 $\pm$ 0.5	13.6 $\pm$ 3.0
AVMU 16104	5	42.2 $\pm$ 2.0	75.1 $\pm$ 2.7	37.1 $\pm$ 3.1	21.4 $\pm$ 4.1	8.1 $\pm$ 0.2	8.1 $\pm$ 0.5	13.7 $\pm$ 3.0
AVMU 16105	6	42.9 $\pm$ 2.0	76.4 $\pm$ 2.7	36.2 $\pm$ 3.1	27.8 $\pm$ 4.1	7.7 $\pm$ 0.2	8.3 $\pm$ 0.5	19.2 $\pm$ 3.0
AVMU 1677	7	42.0 $\pm$ 2.0	76.5 $\pm$ 2.7	37.6 $\pm$ 3.1	21.7 $\pm$ 4.1	7.7 $\pm$ 0.2	9.0 $\pm$ 0.5	15.4 $\pm$ 3.0
AVMU 1678	8	42.5 $\pm$ 2.0	77.2 $\pm$ 2.7	36.5 $\pm$ 3.1	24.4 $\pm$ 4.1	7.7 $\pm$ 0.2	8.7 $\pm$ 0.5	16.9 $\pm$ 3.0
AVMU 1679	9	42.7 $\pm$ 2.0	75.4 $\pm$ 2.7	35.5 $\pm$ 3.1	21.3 $\pm$ 4.1	7.5 $\pm$ 0.2	8.4 $\pm$ 0.5	15.5 $\pm$ 3.0
AVMU 1680	10	43.0 $\pm$ 2.0	75.5 $\pm$ 2.7	37.5 $\pm$ 3.1	19.2 $\pm$ 4.1	7.8 $\pm$ 0.2	9.4 $\pm$ 0.5	15.4 $\pm$ 3.0
AVMU 1681	11	42.5 $\pm$ 2.0	75.3 $\pm$ 2.7	37.5 $\pm$ 3.1	32.3 $\pm$ 4.1	7.3 $\pm$ 0.2	9.7 $\pm$ 0.5	21.8 $\pm$ 3.0
AVMU 1682	12	41.5 $\pm$ 2.0	74.5 $\pm$ 2.7	31.8 $\pm$ 3.1	17.9 $\pm$ 4.1	7.0 $\pm$ 0.2	8.2 $\pm$ 0.5	10.5 $\pm$ 3.0
AVMU 1683	13	42.7 $\pm$ 2.0	75.9 $\pm$ 2.7	34.4 $\pm$ 3.1	19.1 $\pm$ 4.1	7.4 $\pm$ 0.2	7.8 $\pm$ 0.5	10.5 $\pm$ 3.0
AVMU 1684	14	42.6 $\pm$ 2.0	75.7 $\pm$ 2.7	39.0 $\pm$ 3.1	23.5 $\pm$ 4.1	7.7 $\pm$ 0.2	8.4 $\pm$ 0.5	13.6 $\pm$ 3.0
AVMU 1685	15	41.7 $\pm$ 2.0	74.5 $\pm$ 2.7	33.6 $\pm$ 3.1	18.6 $\pm$ 4.1	7.2 $\pm$ 0.2	8.1 $\pm$ 0.5	12.7 $\pm$ 3.0
AVMU 1686	16	41.3 $\pm$ 2.0	74.9 $\pm$ 2.7	34.6 $\pm$ 3.1	24.5 $\pm$ 4.1	6.9 $\pm$ 0.2	7.9 $\pm$ 0.5	11.9 $\pm$ 3.0
AVMU 1687	17	41.8 $\pm$ 2.0	75.7 $\pm$ 2.7	34.3 $\pm$ 3.1	19.2 $\pm$ 4.1	7.6 $\pm$ 0.2	8.3 $\pm$ 0.5	11.0 $\pm$ 3.0
AVMU 1688	18	42.9 $\pm$ 2.0	76.3 $\pm$ 2.7	37.5 $\pm$ 3.1	21.0 $\pm$ 4.1	7.9 $\pm$ 0.2	8.2 $\pm$ 0.5	15.2 $\pm$ 3.0
AVMU 1689	19	42.0 $\pm$ 2.0	75.8 $\pm$ 2.7	37.5 $\pm$ 3.1	23.4 $\pm$ 4.1	7.8 $\pm$ 0.2	8.7 $\pm$ 0.5	16.6 $\pm$ 3.0
AVMU 1690	20	43.0 $\pm$ 2.0	77.1 $\pm$ 2.7	35.1 $\pm$ 3.1	20.4 $\pm$ 4.1	7.8 $\pm$ 0.2	8.5 $\pm$ 0.5	15.3 $\pm$ 3.0
AVMU 1694	21	42.3 $\pm$ 2.0	75.4 $\pm$ 2.7	33.2 $\pm$ 3.1	21.9 $\pm$ 4.1	8.1 $\pm$ 0.2	8.2 $\pm$ 0.5	13.3 $\pm$ 3.0
AVMU 1695	22	42.0 $\pm$ 2.0	74.8 $\pm$ 2.7	33.3 $\pm$ 3.1	21.6 $\pm$ 4.1	7.6 $\pm$ 0.2	7.7 $\pm$ 0.5	12.3 $\pm$ 3.0
AVMU 1696	23	42.0 $\pm$ 2.0	75.6 $\pm$ 2.7	35.0 $\pm$ 3.1	25.1 $\pm$ 4.1	7.6 $\pm$ 0.2	8.1 $\pm$ 0.5	15.2 $\pm$ 3.0
AVMU 1697	24	42.2 $\pm$ 2.0	74.9 $\pm$ 2.7	34.0 $\pm$ 3.1	18.6 $\pm$ 4.1	7.9 $\pm$ 0.2	8.9 $\pm$ 0.5	15.4 $\pm$ 3.0
AVMU 1698	25	41.9 $\pm$ 2.0	75.0 $\pm$ 2.7	37.2 $\pm$ 3.1	20.4 $\pm$ 4.1	7.7 $\pm$ 0.2	8.4 $\pm$ 0.5	12.4 $\pm$ 3.0
AVMU 1699	26	42.7 $\pm$ 2.0	76.1 $\pm$ 2.7	33.8 $\pm$ 3.1	30.6 $\pm$ 4.1	6.9 $\pm$ 0.2	9.0 $\pm$ 0.5	15.5 $\pm$ 3.0
Genotype	Gen#	SY	SW_100	SYHa	Dry matter	Ca	Fe	Zn
AVMU 16100	1	7.6 $\pm$ 1.1	4.2 $\pm$ 0.2	1288.8 $\pm$ 171.3	87.2 $\pm$ 0.2	132.5 $\pm$ 6.2	7.3 $\pm$ 0.4	2.8 $\pm$ 0.2
AVMU 16101	2	7.6 $\pm$ 1.1	4.0 $\pm$ 0.2	1311.4 $\pm$ 168.3	87.3 $\pm$ 0.2	133.4 $\pm$ 6.2	7.1 $\pm$ 0.4	2.6 $\pm$ 0.2
AVMU 16102	3	8.5 $\pm$ 1.1	4.7 $\pm$ 0.2	1482.1 $\pm$ 168.5	87.3 $\pm$ 0.2	115.6 $\pm$ 6.2	6.9 $\pm$ 0.4	2.8 $\pm$ 0.2
AVMU 16103	4	7.9 $\pm$ 1.1	4.8 $\pm$ 0.2	1470.8 $\pm$ 168.3	87.4 $\pm$ 0.2	126.3 $\pm$ 6.2	7.3 $\pm$ 0.4	2.7 $\pm$ 0.2
AVMU 16104	5	8.2 $\pm$ 1.1	4.8 $\pm$ 0.2	1504.1 $\pm$ 168.8	87.3 $\pm$ 0.2	120.5 $\pm$ 6.2	6.9 $\pm$ 0.4	2.7 $\pm$ 0.2
AVMU 16105	6	8.4 $\pm$ 1.1	4.6 $\pm$ 0.2	1489.3 $\pm$ 172.6	87.4 $\pm$ 0.2	120.2 $\pm$ 6.2	7.7 $\pm$ 0.4	2.7 $\pm$ 0.2
AVMU 1677	7	8.6 $\pm$ 1.1	5.0 $\pm$ 0.2	1391.5 $\pm$ 171.3	87.1 $\pm$ 0.2	133.0 $\pm$ 6.2	7.3 $\pm$ 0.4	2.6 $\pm$ 0.2
AVMU 1678	8	7.7 $\pm$ 1.1	4.9 $\pm$ 0.2	1355.7 $\pm$ 168.3	87.1 $\pm$ 0.2	125.7 $\pm$ 6.2	6.9 $\pm$ 0.4	2.7 $\pm$ 0.2
AVMU 1679	9	7.0 $\pm$ 1.1	4.7 $\pm$ 0.2	1215.9 $\pm$ 171.5	87.2 $\pm$ 0.2	132.0 $\pm$ 6.2	7.4 $\pm$ 0.4	2.8 $\pm$ 0.2
AVMU 1680	10	7.9 $\pm$ 1.1	4.8 $\pm$ 0.2	1414.5 $\pm$ 168.3	87.3 $\pm$ 0.2	121.1 $\pm$ 6.2	7.5 $\pm$ 0.4	2.9 $\pm$ 0.2
AVMU 1681	11	8.2 $\pm$ 1.1	4.6 $\pm$ 0.2	1357.8 $\pm$ 172.2	87.2 $\pm$ 0.2	123.7 $\pm$ 6.2	7.1 $\pm$ 0.4	2.6 $\pm$ 0.2
AVMU 1682	12	6.0 $\pm$ 1.1	4.6 $\pm$ 0.2	1023.1 $\pm$ 168.4	87.3 $\pm$ 0.2	123.7 $\pm$ 6.2	7.4 $\pm$ 0.4	2.9 $\pm$ 0.2
AVMU 1683	13	6.3 $\pm$ 1.1	4.8 $\pm$ 0.2	957.2 $\pm$ 168.5	87.3 $\pm$ 0.2	124.6 $\pm$ 6.2	7.5 $\pm$ 0.4	2.8 $\pm$ 0.2
AVMU 1684	14	7.1 $\pm$ 1.1	4.5 $\pm$ 0.2	1242.5 $\pm$ 168.7	87.3 $\pm$ 0.2	123.4 $\pm$ 6.2	8.1 $\pm$ 0.4	2.7 $\pm$ 0.2
AVMU 1685	15	6.6 $\pm$ 1.1	4.4 $\pm$ 0.2	1238.0 $\pm$ 168.3	87.2 $\pm$ 0.2	128.6 $\pm$ 6.2	7.2 $\pm$ 0.4	2.8 $\pm$ 0.2
AVMU 1686	16	6.8 $\pm$ 1.1	4.0 $\pm$ 0.2	1160.7 $\pm$ 168.4	87.2 $\pm$ 0.2	133.1 $\pm$ 6.2	7.4 $\pm$ 0.4	2.9 $\pm$ 0.2
AVMU 1687	17	7.0 $\pm$ 1.1	5.0 $\pm$ 0.2	1188.1 $\pm$ 168.5	87.3 $\pm$ 0.2	115.8 $\pm$ 6.2	7.4 $\pm$ 0.4	2.8 $\pm$ 0.2
AVMU 1688	18	7.5 $\pm$ 1.1	4.9 $\pm$ 0.2	1412.1 $\pm$ 168.5	87.2 $\pm$ 0.2	111.8 $\pm$ 6.1	7.1 $\pm$ 0.4	2.8 $\pm$ 0.2
AVMU 1689	19	7.8 $\pm$ 1.1	4.8 $\pm$ 0.2	1408.4 $\pm$ 171.2	87.3 $\pm$ 0.2	117.1 $\pm$ 6.2	6.6 $\pm$ 0.4	2.7 $\pm$ 0.2
AVMU 1690	20	7.4 $\pm$ 1.1	4.9 $\pm$ 0.2	1197.5 $\pm$ 171.2	87.2 $\pm$ 0.2	121.7 $\pm$ 6.2	6.6 $\pm$ 0.4	2.7 $\pm$ 0.2
AVMU 1694	21	6.8 $\pm$ 1.1	4.9 $\pm$ 0.2	1241.3 $\pm$ 168.3	87.4 $\pm$ 0.2	116.1 $\pm$ 6.2	7.3 $\pm$ 0.4	2.8 $\pm$ 0.2
AVMU 1695	22	6.4 $\pm$ 1.1	4.6 $\pm$ 0.2	1125.5 $\pm$ 168.3	87.4 $\pm$ 0.2	121.0 $\pm$ 6.2	7.3 $\pm$ 0.4	2.8 $\pm$ 0.2
AVMU 1696	23	6.9 $\pm$ 1.1	4.3 $\pm$ 0.15	1314.4 $\pm$ 168.4	87.2 $\pm$ 0.2	133.4 $\pm$ 6.3	7.7 $\pm$ 0.4	2.9 $\pm$ 0.2
AVMU 1697	24	6.5 $\pm$ 1.1	4.7 $\pm$ 0.2	1155.6 $\pm$ 171.2	87.3 $\pm$ 0.2	116.5 $\pm$ 6.1	7.6 $\pm$ 0.4	2.7 $\pm$ 0.2
AVMU 1698	25	6.7 $\pm$ 1.1	5.0 $\pm$ 0.2	1210.4 $\pm$ 168.5	87.4 $\pm$ 0.2	116.6 $\pm$ 6.2	7.7 $\pm$ 0.4	2.9 $\pm$ 0.2
AVMU 1699	26	7.5 $\pm$ 1.1	4.1 $\pm$ 0.2	1265.7 $\pm$ 168.4	87.2 $\pm$ 0.2	122.1 $\pm$ 6.2	6.8 $\pm$ 0.4	2.7 $\pm$ 0.2

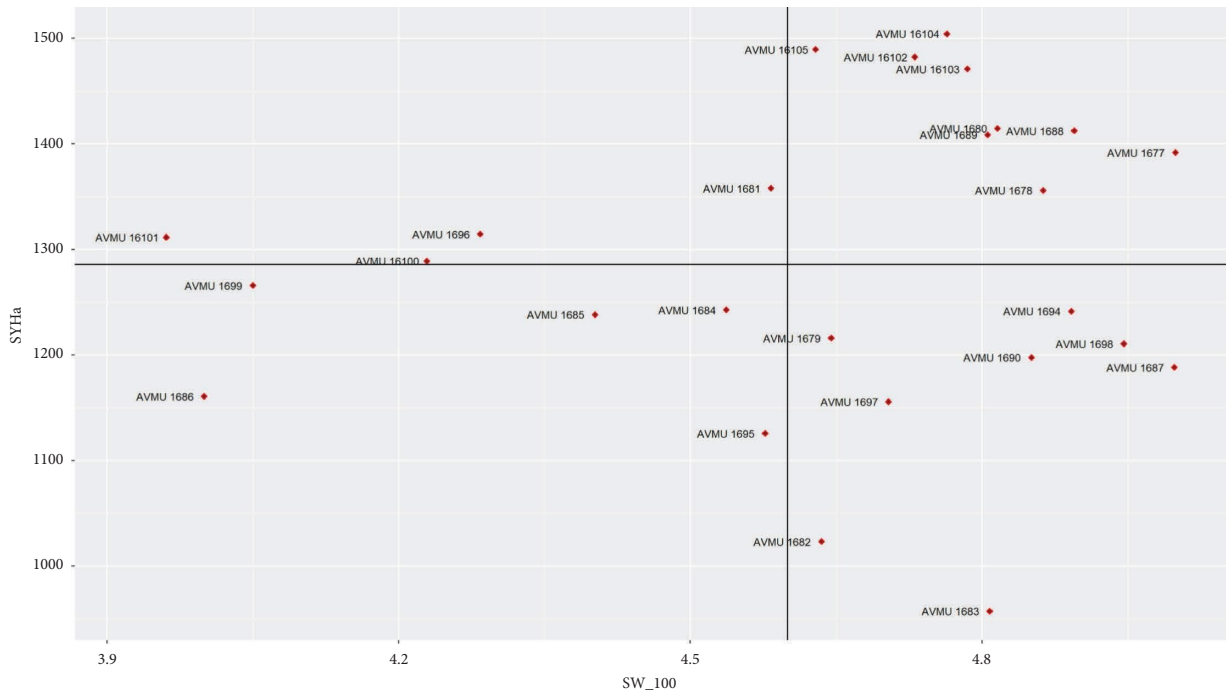


FIGURE 3: Comparison of seed yield/ha and seed size among elite mungbean genotypes.

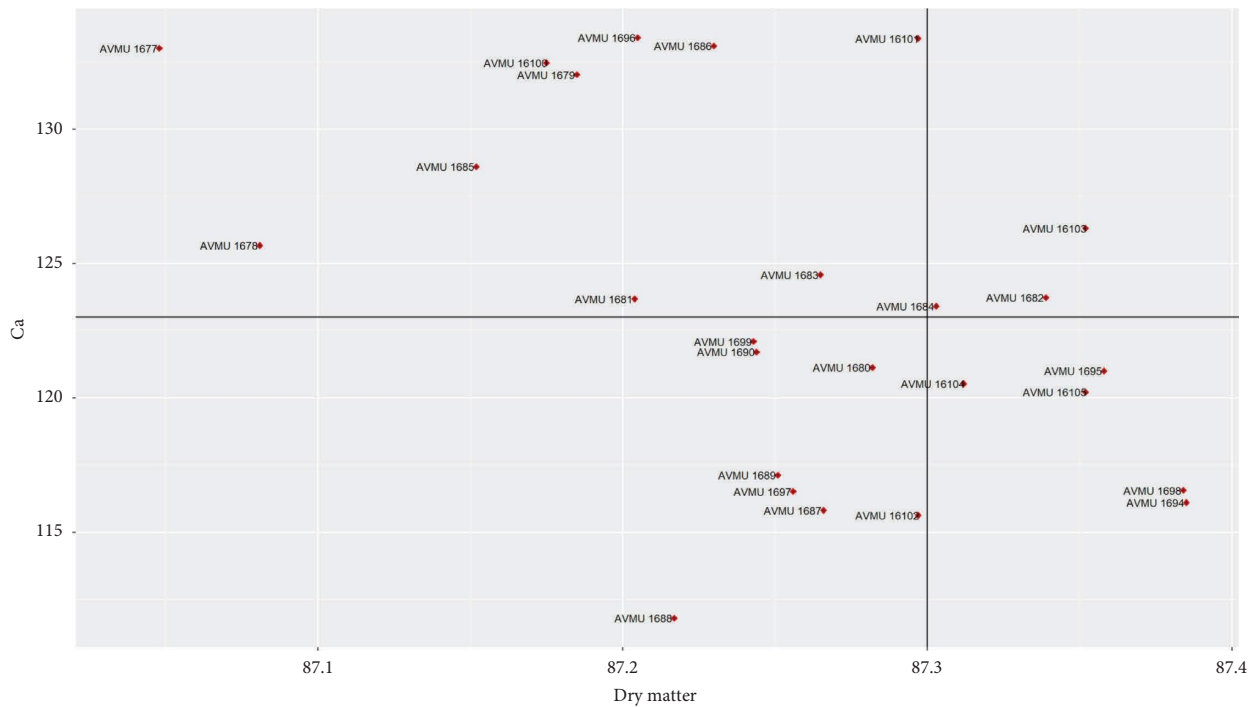


FIGURE 4: Comparison of calcium (Ca) and dry matter contents among mungbean genotypes.

environments with a higher concentration of available soil nutrients also had high levels of nutrients in the grains/seeds. This was especially observed for iron and zinc.

Broad-sense heritability for DFF, DM, PH, NP, PL, NS, PY, SY, SW\_100, SYHa, dry matter, calcium, iron, and zinc was 45%, 68%, 41%, 56%, 83%, 62%, 45%, 26%, 84%, 38%, 10%, 74%, 49%, and 48%, respectively (Table 5). Among the

nutrient traits, dry matter content had the lowest heritability while calcium had the highest heritability. There were small differences between heritability for iron and zinc contents in the test environments. Among agronomic traits, yield per plant had the lowest heritability followed by yield per hectare. Pod length and one hundred seed weight had the highest heritability estimates.

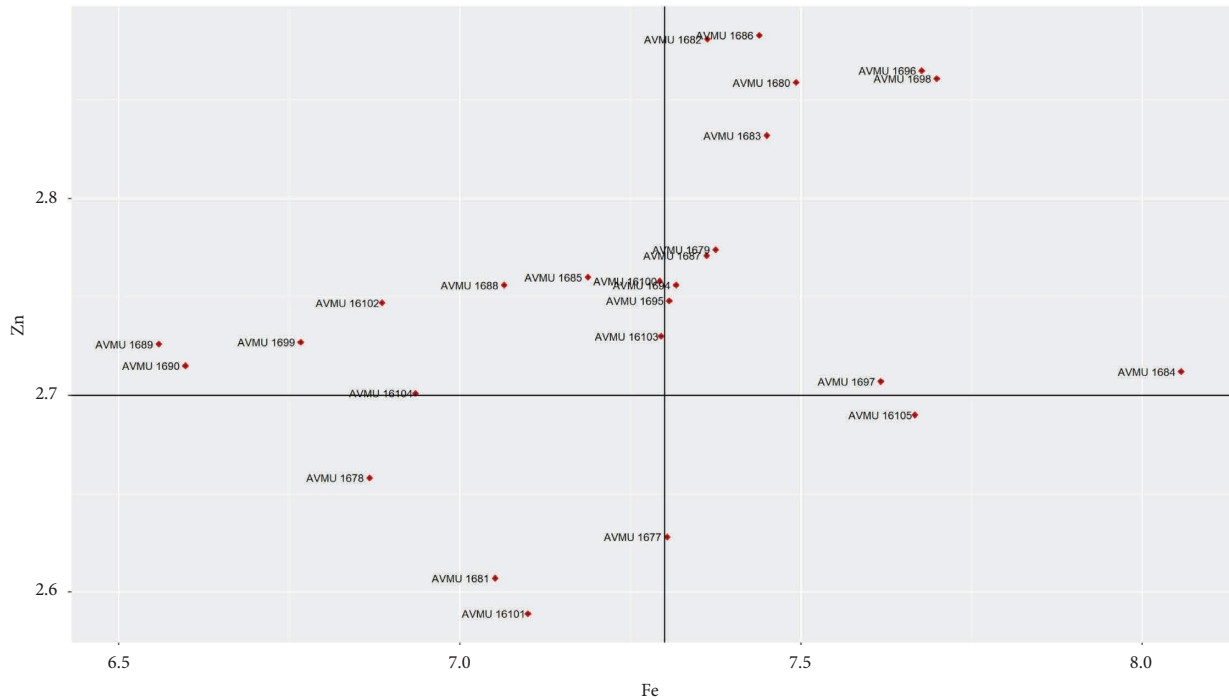


FIGURE 5: Comparison of iron (Fe) and zinc (Zn) among mungbean genotypes.

Of the 26 elite genotypes, only nine had the best combination of high yield and large seed size (100 seed weights) with 100 seed weights greater than the average mean (4.6 g). These were AVMU 16105, AVMU 16104, AVMU 16102, AVMU 16103, AVMU 1680, AVMU 1689, AVMU 1688, AVMU 1677, and AVMU 1678 (Table 6 and Figure 3). AVMU 1683 was the lowest yielding genotype, while AVMU 16101 and AVMU 1686 had the smallest seed sizes.

In terms of calcium and dry matter composition, only three elite genotypes gave the best combination of high calcium levels and high dry matter content. These were AVMU 16103, AVMU 1682, and AVMU 1684 (Table 6 and Figure 4). The genotypes with the highest dry matter levels were AVMU 1698 and AVMU 1694, while AVMU 1677 was the lowest. For calcium content, AVMU 1677, AVMU 1696, AVMU 86, and AVMU 16101 had the highest levels.

For iron and zinc contents, twelve elite genotypes had both high zinc and iron levels with values above the overall mean for both minerals. These were AVMU 1682, AVMU 1686, AVMU 1680, AVMU 1696, AVMU 1698, AVMU 1683, AVMU 1679, AVMU 1694, AVMU 1687, AVMU 1695, AVMU 1697, and AVMU 1684. The genotype with the highest iron content was AVMU 1684, while the genotype with the lowest iron level was AVMU 1689. For zinc content, the genotype with the highest level was AVMU 1686 while the one with the lowest level was AVMU 16101 (Table 6 and Figure 5).

**3.3. Variance Components for Agronomic Traits and Mineral Composition across Seasons.** Results from a combined analysis of variance, fixed effect of genotype effect, and variance components for environment and genotype ( $G$ )  $\times$  environment ( $E$ ) interactions are presented in Table 7.

Significant genotype effects were observed for most of the traits except for seed yield per plant and dry matter. The random effect of environment was significant for all traits, and significant GXE was observed for all traits except for dry matter and iron content (Table 7).

**3.4. Yield and Mineral Stability among Genotypes across Environments.** Biplot analysis was carried out for yield and nutrient composition traits except for nonsignificant  $G \times E$  of dry matter content and iron content. Biplot analysis for yield trait divided the test environments into 5 mega-environments (Figure 6). The first mega-environment comprised of TARI\_Ukiriguru\_2019B and Serere\_2019B with AVMU 1686 as the winning or highest yielding genotype. These two environments had low discrimination power, i.e., both locations do not provide enough information on variation among genotypes. The second mega-environment comprised of KAT\_LR\_2020, Ithookwe\_LR\_2020, KYM\_LR\_2020, and KYM\_SR\_2019 with AVMU 16101 as the most prominent genotype. In this mega-environment, KYM had more discriminating power (i.e., more informative) for both LR\_2020 and SR\_2019 compared with the rest of the two environments. The third mega-environment comprised of Arua\_2019B, KAT\_SR\_2019, Lira\_2020A, Serere\_2020A, Miwaleni\_2019B, WVC\_Tengeru\_2019B, and Lira\_2020A with AVMU 16105 as the specific adaptable genotype for this particular mega-environment. In this mega-environment, KAT\_SR\_2019 had moderate discriminating power while the rest were nondiscriminating. The fourth mega-environment consisted of only Ithookwe\_SR\_2019 with AVMU 1696 as the winning genotype, and this environment had high discriminating power. The fifth mega-

TABLE 7: Combined analysis of variance of fixed ( $F$  value) and random effects (variance components) for mungbean genotypes across 15 environments.

Effect	DF	Fixed effect ( $F$ value)					
		DM	PH	NP	PL	NS	PY
Genotype	2.21**	3.10**	1.70*	2.25**	5.86**	2.45**	1.795*
Random effects (variance components)							
ENV	55.26**	105.42**	94.42**	165.83**	0.45**	1.41**	61.95**
Rep (Env)	0 <sup>ns</sup>	0.014 <sup>ns</sup>	1.29*	1.35**	0.06**	0.15**	0.005 <sup>ns</sup>
Env * Gen	1.19**	1.793**	25.34**	74.08**	0.13**	0.76**	38.61**
Residual	80.28	44.75	174.05	316.44	7.09	9.54	26.11
Effect	SY	Fixed effect ( $F$ value)					
		SW100	SYHa	DryMatter	Ca	Fe	Zn
Genotype	1.4 <sup>ns</sup>	6.51**	1.60*	1.24 <sup>ns</sup>	3.95**	2.48**	2.01**
Random effect (variance components)							
ENV	11.55**	0.138**	239071.15**	0.215**	271.11**	0.922**	0.211**
Rep (Env)	0.088**	0.004 <sup>ns</sup>	3049.59**	0.037**	3.839 <sup>ns</sup>	0 <sup>ns</sup>	0.005**
Env * Gen	4.3**	0.128**	170543.42**	0.008 <sup>ns</sup>	50.78**	0.065 <sup>ns</sup>	0.009**
Residual	83.81	8.96	38993.52	1.777	1545.73	19.08	0.69

ENV: environment, environment  $\times$  replicate interaction, Env  $\times$  Gen: environment  $\times$  genotype interaction, DFF: no. of days to 50% flowering, DM: no. of days to 90% pod maturity, PH: plant height, PL: pod length, NP: no. of pods/plant, NS: no. of seeds per pod, PY: pod weight/plant, SY: seed weight/plant, SW\_100: weight of 100 seeds, SYHa: grain yield/ha, ns: nonsignificant, and \* and \*\*: significant at 5% and 0.1%, respectively.

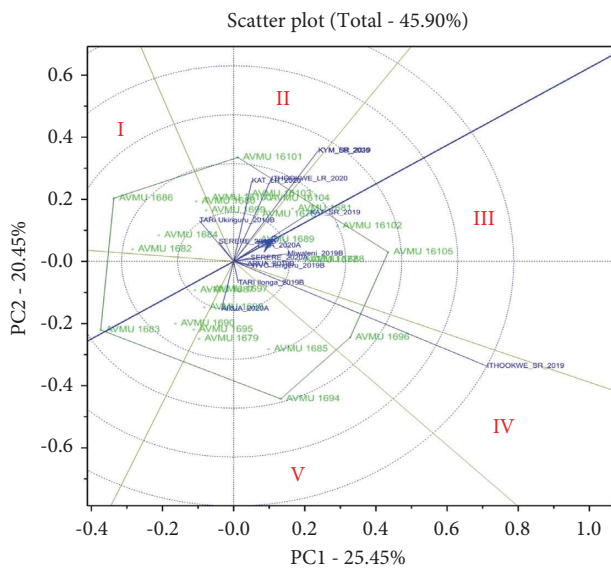


FIGURE 6: Biplot analysis for grain yield of elite mungbean genotypes evaluated in the study.

environment was comprised of Arua\_2020A and TARI\_Ilonga\_2019B, and these had very low discriminating power and can not be recommended for future experimental trials.

Among the 26 mungbean genotypes, the genotypes with both high average yield performance and stability (genotypes nearer to the AEA axis) were AVMU 1689, AVMU 1681, and AVMU 16102 as these were closer to the ideal genotype in the center of the concentric circles and in the positive direction of AEA (Figure 6). Crossover interactions were identified between TARI\_Ukiriguru\_2019B and ITHOOKWE\_SR\_2019, i.e., genotype ranks changing with

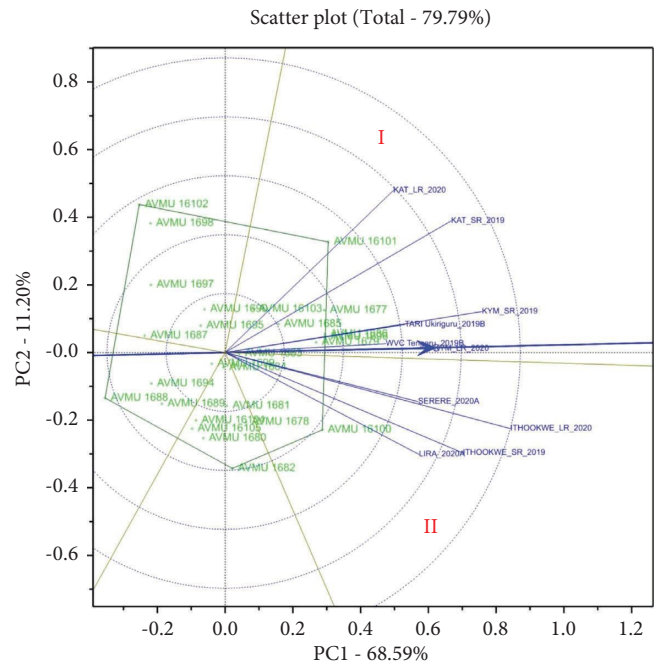


FIGURE 7: Biplot analysis for calcium content of elite mungbean genotypes evaluated in the study.

the extreme environments in the biplot were identified as indicated by the presence of wide obtuse angles ( $\theta > 90^\circ$ ).

Biplot view of calcium content among genotypes across test environments identified two mega-environments. The first mega-environment comprised of KAT\_LR\_2020, KAT\_SR\_2019, KYM\_SR\_2019, TARI\_Ukiriguru\_2019B, WVC, Tengeru\_2019B, and KYM\_LR\_2020. In this mega-environment, the genotype with the highest calcium content was AVMU 16101 (Figure 7).

The second mega-environment was comprised of Serere\_2020A, Ithookwe\_LR\_2020, Ithookwe\_SR\_2019, and Lira\_2020A with AVMU 16100 as the winning genotype. The most discriminating environments were Ithookwe\_LR\_2020 > KYM\_SR\_2019 > KAT\_SR\_2019 > Ithookwe\_SR\_2019 as indicated by their long vectors. However, no environment was found to be both discriminating and representative regarding calcium content. The most suitable genotypes with high average performance and stable calcium content were AVMU 1683, AVMU 1679, AVMU 1696, AVMU 1686, and AVMU 1685 (Figure 7). There was no crossover interaction among test environments, i.e., genotype ranks do not change much across environments, and the angle between the two extreme environments (KAT\_LR\_2020 and LIRA\_2020A) was acute ( $\theta < 90^\circ$ ).

Biplot analysis for zinc content partitioned the test environments into three mega-environments (Figure 8). The first mega-environment comprised of Ithookwe\_SR\_2019, KYM\_SR\_2019, TARI, Ukiriguru\_2019B, WVC, Tengeru\_2019B, KAT\_SR\_2019, and KYM\_LR\_2020. In this mega-environment, the winning genotypes were AVMU 1696 and AVMU 1682. The second mega-environment was comprised of Serere\_2020A and Lira\_2020A with AVMU 1686 as the winning genotype. The third mega-environment was comprised of KAT\_LR\_2020 and Ithookwe\_LR\_2020 with AVMU 1698 as the winning genotype. KYM\_SR\_2019 was the most discriminating environment, while KYM\_LR\_2020 was considered an ideal test environment because of its high discriminating power and representativeness. Regarding high zinc content and stability, the genotypes AVMU 1686 > AVMU 1682 had high average performance, and stable genotypes were AVMU 1679 and AVMU 1685. There were no crossover interactions among test environments with genotype rank not changing much, and the angle between the two extreme environments (Ithookwe\_SR\_2019 and Ithookwe\_LR\_2020) was acute angle ( $\theta < 90^\circ$ ).

**3.5. Relationship between Yield, Seed Size, and Mineral Composition.** Correlation analysis showed that grain yield was significantly ( $\text{prob} < 0.05$ ) and negatively correlated with zinc and calcium contents but nonsignificantly correlated ( $\text{prob} \geq 0.05$ ) with iron content (Table 8). Grain yield was not correlated with 100 seed weight and dry matter content. Although iron, calcium, and dry matter contents were negatively correlated with SW\_100, only calcium showed a strong and negative significant correlation. Iron content had a significant positive correlation with zinc and calcium contents.

## 4. Discussion

**4.1. Soil Physico-Chemical Characteristics.** Soil texture at most of the trial sites was sandy clay loam with pH ranging from 5.1 at Ithookwe, Kenya, to 7.52 at Miwaleni, Tanzania. According to Horneck et al. [16], the pH range at the trial sites is broadly categorized as strongly acidic ( $\leq 5.1$ ) to

moderately alkaline (7.4–8.4). Well-drained loamy to sandy loam soils with a slightly acidic to neutral soil pH are the most ideal for mungbean cultivation since such soils tend to have good drainage [17, 18]. While mungbean can grow in soils with a wide pH range, different varieties/genotypes tend to have specific optimal pH levels [19]. The soils were generally deficient in nitrogen and organic carbon content based on the criteria proposed by Horneck et al. [16]. A similar trend was observed for P at Uganda sites ( $< 20$  ppm) and for K in Uganda and Tanzania. Micronutrient levels (iron and zinc) were generally sufficient for mungbean growth. According to Horneck et al. [16], micronutrient availability tends to increase as soil pH reduces. Nair et al. [3] observed an increase in available soil iron and zinc levels with a reduction in soil pH. However, in our findings, the highest iron levels were obtained at moderately alkaline pH. Soil zinc levels of  $> 1.5$  ppm are considered sufficient for most crops [16].

**4.2. Genetic Effect on Agronomic Traits and Nutrient Composition.** In this study, mungbean genotypes showed significant variation for all traits except iron and dry matter contents (Table 7). A considerable range for both agronomic traits and nutrient composition was observed among the mungbean genotypes. Variation in iron levels ranged from 6.6 to 8.1 mg/100 g for AVMU 1684 and AVMU 1689, respectively, while zinc ranged from 2.6 to 2.9 mg/100 g for AVMU 16101 and AVMU 1686, respectively. Singh [20] and Singh et al. [21] reported a variation of 1.6–9.2 mg/100 g for iron and a range of 1.54–3.57 mg/100 g for zinc. Calcium content among genotypes ranged from 111.8 mg/100 g to 133.4 mg/100 g. Nair et al. [3] reported a range of 2.1–6.2 mg/100 g for zinc and 3.5–8.7 mg/100 g for iron in mungbean. Vijayalakshmi et al. [22], however, reported a lower range of 3.3–6.0 mg/100 g for iron content. This could be attributed to the small number of genotypes (four) that were evaluated. High iron and calcium levels of up to 8.7 mg/100 g and 158 mg/100 g in genotypes CN 9-5 and Harsha, respectively, were reported by Nair et al. [3]. It is important to note that mungbean genotypes respond differently to available soil iron levels probably due to differences in the mechanism of iron uptake [3]. Our results also showed great variation for maturity traits (days to 50% flowering and days to maturity), plant height, number of pods/plant, and seed yield per plant compared to those reported by the authors of [20, 21]. Mungbean genotypes evaluated in the current study were generally taller (31.8 cm–39 cm) than the range (22.66–32.98 cm) reported by Mwangi et al. [23]. This could be attributed to differences in the genetic material and geographical regions where the materials were evaluated. Yield and yield component traits are reported to contribute greatly to genetic variation in mungbean [23]. The genotypes used in this study were generally early maturing compared to landraces [24]. Results for seed size (100 seed weight) for the genotypes evaluated in this study are related to those reported by Wani et al. [24]. It is important to note that the test genotypes in this study had small seed size



**4.4. Heritability for Agronomic and Nutrient Traits.** In this study, yield-related traits such as number of pods/plant, pod length, number of seeds/pod, pod weight/plant, seed weight/plant, seed yield per ha, and 100 seed weight gave moderate to high heritability. Yimram et al. [26] also reported moderate to high heritability for seed yield/plant, 100 seed weight, and number of pods/plant in cultivated mungbean. Similar results were reported by Gayacharan et al. [29]. Moderate to high  $H^2$  indicated that a significant proportion of trait variation was due to genetic differences. However, Singh et al. [21] reported lower  $H^2$  values for the number of pods per plant (21.9%) and seed yield per plant (24.3%). Phenology traits such as plant height, days to 50% flowering, and days to maturity also showed moderate  $H^2$  values as previously reported by Singh et al. [21] but lower than those reported by Yimram et al. [26] and Gayacharan et al. [29]. For nutritional (Ca, Fe, Zn) traits, our  $H^2$  estimates were lower than those reported by Nair et al. [3] and Singh et al. [21]. Studies in other legumes such as common bean reported high  $H^2$  for seed/pod and phenology-related traits [31]. Yimram et al. [26] suggested that for traits such as seed and pod traits where the genotypic effect is often greater than the environmental effect and/or genotype  $\times$  interaction effect, improvement could be achieved through selection even at early generations. For traits showing low  $H^2$ , they could be improved through hybridization [31].

**4.5. Relationship between Yield, Seed Size, and Nutrient Contents.** The phenotypic correlation between iron and zinc content was positive and significant ( $r=0.58$ ), indicating a strong association between these micronutrients. Similar results were also reported by earlier studies on mungbean [20, 21]. Carloni et al. [32] also reported a strong and positive association between iron and zinc content in common beans. Similar results were also reported in cowpea by Boukar et al. [33]. The correlation between iron and calcium was also positive and significant. Positive and strong correlations between iron and calcium, iron, and zinc show that selection for any of these traits results in gains for the other as reported for common beans [32]. Correlation analyses between seed size and mineral contents (except for calcium) were nonsignificant, an indication that nutrient content is not affected by seed size. A previous study by Nair et al. [3] also reported no significant association between 100 seed weights and nutrient contents. It is, therefore, possible to develop small or large-seeded mungbean varieties without losing the nutritive value of the grains. No significant correlations were found between yield, iron content, and dry matter content. This is similar to the results reported by Singh [20]. This implies that it is possible to develop mungbean varieties with high iron and dry matter contents without any grain yield penalty. The genetic correlation between yield and zinc was negative, significant, and of strong magnitude ( $r=-0.61$ ). This contrasts with the results reported by Singh [20, 21]. Thus, breeding high yielding varieties may compromise zinc content in the grains. Strong positive associations

between zinc and iron content in grains were also reported in common beans [34, 35]. The correlation between seed size and yield was nonsignificant, contrary to the findings of Waniale et al. [24].

**4.6. Stability Analysis for Yield and Nutrient Composition.** Our results revealed the presence of mega-environments (five for grain yield, two for calcium, and three for zinc content) with different winning genotypes. To confirm the presence of these mega-environments, data from several years are required [15]. Biplot analysis also revealed that Ithookwe\_SR\_2019 was the most discriminating environment for grain yield, while Ithookwe\_LR\_2020 and KYM\_SR\_2019 were the most discriminating for calcium and zinc contents, respectively. Discriminating environments are more informative and are thus very useful for selecting specifically adapted genotypes where target production environments can be divided into mega-environments [15]. On the other hand, environments KAT\_SR\_2019, KYM\_LR\_2020, and Serere\_2020A/KYM\_LR\_2020 were both discriminating and representative for grain yield, calcium, and zinc contents, respectively. Environments that are both discriminating and representative are ideal for selecting generally adapted genotypes [15]. Environments that are consistently nondiscriminating provide little or no information about genotype performance and, therefore, should not be used in genotype evaluation [15]. Such environments should not be included in variety evaluation trials. Biplot analysis identified genotypes AVMU 1679, AVMU 1685, and AVMU 1686 that combined both phenotypic stability as well as high zinc and calcium contents. A similar study by Araujo et al. [36] showed the suitability of biplots in selecting adaptable and stable cowpea genotypes for micronutrients and protein content. However, the most desirable genotypes for high yield and yield stability were dissimilar (AVMU 1689, AVMU 1681, and AVMU 16102).

## 5. Conclusions

This study revealed the presence of significant differences among mungbean genotypes for all traits except SY and dry matter contents. Genotype  $\times$  environment interaction was nonsignificant for iron and dry matter contents. Desirable genotypes such as AVMU 1679, AVMU 1685, and AVMU 1686 that combined both phenotypic stability and high zinc/calcium content were identified in this study. Similarly, high yielding and stable genotypes (AVMU 1689, AVMU 1681, and AVMU 16102) were identified. However, the genotypes tested were small-seeded (with SW\_100 less than 5 g), yet large seed size is one of the key traits that farmers often consider in variety selection in East Africa. On-farm trials are recommended to assess farmer preference or nonpreference for these identified genotypes before they can be considered for release as new varieties. Significant and positive correlations between Fe, Zn, and Ca indicate the potential to enhance these traits simultaneously through breeding.

## Data Availability

The data presented for this study can be availed on request from the corresponding author.

## Disclosure

The funders had no role in the design of the study; in the collection, analysis, or interpretation of the data; in the writing of the manuscript; or in the decision to publish the results.

## Conflicts of Interest

The authors declare that there are no conflicts of interest.

## Authors' Contributions

E.K.M., R.K., P.H.B., and R.M.N. conceptualized the study; E.K.M., R.K., P.H.B., and R.M.N. provided methodology; E.K.M. and A.K.V. developed software; E.K.M. and A.K.V. performed formal analysis; E.K.M., R.K., E.S.A., P.H.B., and R.M.N. investigated the study; E.K.M., R.K., P.H.B., and R.M.N. collected resources; E.K.M. and A.K.V. curated data; E.K.M. wrote the original draft; E.K.M., R.K., E.S.A., P.H.B., R.M.N., and A.K.V. wrote the manuscript and reviewed and edited the manuscript; E.K.M. visualized the study; E.K.M. administrated the project; E.K.M. contributed funding acquisition. All authors have read and agreed to the published version of the manuscript.

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## Supplementary Materials

S1: Variation in the number of days to 50% flowering (DFF), plant height (PH), number of pods per plant (NP), and pod length across environments. S2: Variation in pod yield per plant (PY), seed yield per plant (SY), number of seeds per pod (NS), and weight of 100 seeds (SW\_100) across environments. S3: Variation in calcium and dry matter contents among genotypes across environments. (*Supplementary Materials*)

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